IN THE CLAIMS

The claims are amended as follows:

1. (canceled)

2. (canceled)

3. (canceled)

4. (canceled)

5. (canceled)

6. (canceled)

7. (canceled)

8. (canceled)

9. (canceled)

10. (canceled)

11. (canceled)

12. (canceled)

13. (canceled)

14. (canceled)

15. (canceled)

16. (canceled)

17. (canceled)

18. (canceled)

19. (new) A method of using a trainable system for predicting pairwise interactions of biopolymers, the method comprising the steps of:

inputting a database of known biomolecular pairwise interactions as a set of features on a residue-by-residue basis;

representing the biopolymers as a linear set of features;

training the system to learn patterns based on these features that are associated with the propensity for interaction;

inputting to the trained system a set of features representing query biopolymers whose interactions are not known; and

outputting predicted interaction pairs from the query data.

20. (new) The method of claim 19, wherein said biopolymers are selected from the group consisting of proteins and nucleic acids.

21. (new) The method of claim 19, wherein said training comprises sliding a window along a sequence of features, each step outputting a numerical value that constitutes a pairwise interaction value of one or more members of a sequence within a window;

22. (new) The method of claim 19, wherein said query biopolymer is selected from the group consisting of proteins, nucleic acids, and small molecules.

23. (new) The method of claim 19, wherein said interaction pairs are selected from the group consisting of small molecule-protein, small molecule-nucleic acid, protein-protein, and protein-nucleic acid.

24. (new) The method of claim 19, wherein the trainable system is a support vector machine.

25. (new) The method of claim 19, wherein feature vectors are assembled from encoded representations of residue properties.

26. (new) The method of claim 19, wherein the set of features is not a limiting aspect of the invention, instead any set of physical, chemical or biological features corresponding in a discrete or spatially-averaged sense to each residue or nucleotide in a linear biopolymer sequence may be used to construct an example for training the system.

27. (new) The method of claim 26, wherein the set of features are concatenated to create an interaction pair example.

28. (new) The method of claim 19, wherein the output quantity represents a molecular binding energy between the interaction pairs.

29. (new) The method of claim 21, further comprising the step of outputting a threshold score indicative of the local propensity for binding of one or more members of each sequence along which the window slid.